REMARKS/ARGUMENTS

Reconsideration of this patent application is respectfully requested in view of the foregoing amendments, and the following remarks. Claims 1-8 are in the application. Claims 3, 6 and 7 have been amended. The specification and sequence listing have been amended. No new matter has been added.

The Examiner requested that a typed version of Form 1449 from the Information Disclosure Statement be submitted. Applicants submit herewith a typed version of the form, containing a listing of the references already submitted.

The Examiner objected to the specification for lacking headings and a brief description of FIG. 1. Applicants have amended the specification to add headings and to include a description of FIG. 1.

The Examiner objected to the sequence listing, stating that the CRF copy submitted is flawed. Applicants submit herewith a corrected CRF copy of the sequence listing, and the required statement.

The Examiner objected to claim 3 for referring to a Table. Applicants have amended claim 3 in accordance with the Examiner's suggestions, to include a listing of the specific mutations from the table.

The Examiner rejected claims 6-8 under 35 U.S.C. §112, stating that the plasmid of claims 6-8 must be obtainable or available. Applicants submit that a deposit of the plasmid of claims 6-8 was not made because the plasmid is easily reproducible by one of skill in the art. The plasmid of claim 6 can be easily reproduced because the only difference to a known strain is the presence of a metA allele of claim 4. This metA allele is clearly defined in the specification and in claim 4. One of skill in the art can easily make this metA allele, as well as the plasmid containing this metA allele (claim 5), as well as the isolated microbial cell of claims 6 and 7 using standard procedures that have been well known for many years. The examples describe the procedures for the production of several different plasmids, as well as the production of microorganisms using these plasmids (Examples 2 and 3). Therefore, a deposit according to the Budapest treaty is unnecessary for the invention.

The Examiner also rejected claims 6-8 because it was unclear which strain was required. The Examiner suggested amending claims 6-8 to recite "An isolated microbial host cell." Applicants have amended the claims accordingly.

The Examiner has rejected claims 1-8 under 35 U.S.C. §112, first paragraph, as not being sufficiently described in the specification. The Examiner also rejected claims 1-8 under 35 U.S.C. §112, first paragraph, for not being enabled. Applicants respectfully traverse.

The enzyme of claim 1 is defined by the mutation of Asp and Tyr at conserved sites of the protein plus a functional definition (i.e. the reduced sensitivity towards L-methionine or SAM). Some mutants of the wild-type enzyme and the methods to determine the feedback resistance are provided in the description wherein the conserved sites are replaced by various amine acids. Therefore, the scope of claim 1 is appropriate because a person skilled in the art can recognize that the mutants claimed in claim 1 achieve the purpose of the present application.

Therefore, the sequences/proteins according to the present invention can be made by a person skilled in the art using the information of the present specification, and the examples of the present application prove the interrelation of the sequence and the desired features. Enclosed as Appendix A is an alignment of the SAM sequences of 14 different species. This alignment shows that in all these enzymes, Asp in position 101 and Tyr in Position 294 (both marked green) are conserved. In the light of this state of the art it is unnecessary to limit claim 1 to SEQ. ID. No.: 2, as claim 1 as written is in compliance with 35 USC §112.
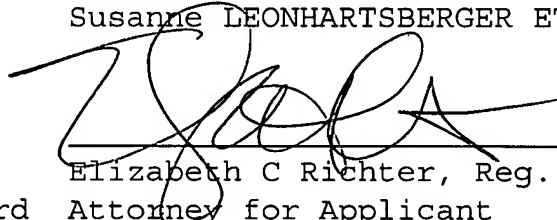
The Examiner rejected claims 4 and 5 under 35 U.S.C. §101 for non-statutory subject matter, and suggested that claims 4 and 5 be amended to claim "an isolated nucleic acid encoding homoserine transsuccinylase". Applicants have amended claims 4 and 5 accordingly. Applicants submit that claims 4 and 5 are now in compliance with 35 U.S.C. §101.

The Examiner has rejected claims 1-8 under the judicially-created doctrine of double patenting over claims 1-8 of copending Application Serial No. 10/530,844. Applicants submit herewith a

Terminal Disclaimer, disclaiming that portion of any patent

issuing on the present application that would extend beyond the

term of the patent issuing from application serial no.

10/530,844.

Accordingly, Applicants submit that the application is in

condition for allowance. Early allowance of the claims is

respectfully requested.

Respectfully submitted,
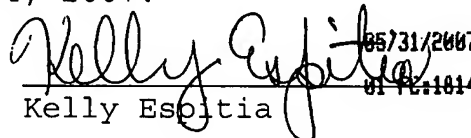Susanne LEONHARTSBERGER ET AL.

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Roslyn, New York 11576
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ECR:cmm

Enclosure: Appendix A
               Corrected Sequence Listing, Disk and Statement
               Terminal Disclaimer and fee
               Typed version of PTO Form 1449

     I hereby certify that this correspondence is being deposited
with the U.S. Postal Service as first class mail in an envelope
addressed to: Commissioner of Patents, P.O. Box 1450, Alexandria,
VA 22313-1450, on May 24, 2007.

Kelly Espitia

05/31/2007 GFKEY1   00000031 10530843
01 FC:1814   130.00 OP

Appendix A

```
                           1                                                  50
MetA_B.halodurans      (1) MPIKIPDNLPAKEILTKENIFVMAESRAYSQDIRPLKIVILNLMPIKQTT
MetA_B.subtilis        (1) MPINIPTHLPAKQVLESEHIFVMDESRAFHQDIRPQKIIILNLMPKKIQT
MetA_Bruc.meritensis   (1) MPIKIPDDLPATSVLEAEGVMVMREADAVRQDIRPLRIGLLNLMPNKVTT
MetA_C.acetobutylicum  (1) MPIKIPDNLPAAKTLNEENIFFMDEDRAYHQDIRPLNIVIVNLMPTKIVT
MetA_Camp.jejuni       (1) MPLIIPENIPAYELLK-EHAFIMGLRRAKHQDIRPQEILIVNLMPKKIET
MetA_E.coli            (1) MPIRVPDELPAVNFLREENVFVMTTSRASGQEIRPLKVLILNLMPKKIET
MetA_L.lactis          (1) MPVKVIEGLPAIDDLRADNIFVMNDERAKNQNIRPLNLLVVNLMPRKLIT
MetA_R.meliloti        (1) MPIKIPDTLPAFETLVHEGVRLMTETEAIRQDIRPLQIGLLNLMPNKIKT
MetA_S.typhi           (1) MPIRVLDELPAVNFLREENVFVMTTSRASGQEIRPLKVLILNLMPKKIET
MetA_S.typhimurium     (1) MPIRVLDELPAVNFLREENVFVMTTSRASGQEIRPLKVLILNLMPKKIET
MetA_Str.pneumoniae    (1) MPIRIDKKLPAVEILRTENIFVMDDQRAAHQDIRPLKILILNLMPQKMVT
MetA_T.maritima        (1) MPINVPSGLPAVKVLAKEGIVMTEKRAIHQDIRPLEILILNLMPDKIKT
MetA_V.cholerae        (1) MPIRIPDQLPASDVLRNENIFVMSESRASTQEIRPLKVLLLNLMPKKIET
MetA_Y.pestis          (1) MPIRVPDELPAVSFLRNENVFVMASSRAKTQEIRPLKVLILNLMPKKIET
Consensus              (1) MPIRIPD LPAV VLR ENIFVM ESRA  QDIRPLKILILNLMPKKI T

                           51                                                 100
MetA_B.halodurans     (51) ETQLLRLLGNTPLQVEVSFMYTDTHISKNTSYDHLQTFYQTIDEVKQKKF
MetA_B.subtilis       (51) ETQLLRLLGNSPLQVHFTFLIPSTHTPKNTAREHLDEFYTTFSNIRHKRF
MetA_Bruc.meritensis  (51) ETQIARLLGATPLQVELTLVRMTNHVARHTPADHMLSFYCPWEEVNDQRF
MetA_C.acetobutylicum (51) ETQILRLIGNSPLQVNPTFIHTQTHKSQNTSKEHLIKFYETFEEIKNNKF
MetA_Camp.jejuni      (50) ENQILSLLANSPLQVNITLLATTSYVGKNTPFTHLEKFYKGLEEVKKHKF
MetA_E.coli           (51) ENQFLRLLSNSPLQVDIQLLRIDSRESRNTPAEHLNNFYCNFEDIQDQNF
MetA_L.lactis         (51) ERQILRLLSNTPLQINVEFLYMTSHDFKNTKQGHLDSFYKSFSEIKSQYY
MetA_R.meliloti       (51) EIQMARLIGATPLQVELTLVRVNGHRPKNTPEEHLLAFYETFEEVEARKF
MetA_S.typhi          (51) ENQFLRLLSNSPLQVDIQLLRIDARESRNTPAEHLNNFYCNFDDICDQNF
MetA_S.typhimurium    (51) ENQFLRLLSNSPLQVDIQLLRIDARESRNTPAEHLNNFYCNFDDICDQNF
MetA_Str.pneumoniae   (51) ETQLLRHLANTPLQLDIDFLYMESHRSKTTRSEHMETFYKTFPEVKDEYF
MetA_T.maritima       (51) EIQLLRLLGNTPLQVNVTLLYTETHKPKHTPIEHILKFYTTFSAVKDRKF
MetA_V.cholerae       (51) ETQFLRLLSNSPLQVDIELLRIDDRPSKNTPEEHLNTFYRQFELVKNRNF
MetA_Y.pestis         (51) ENQFLRLLSKNTPLQLLRVDSRESKNTPTEHLNNFYCDFEDIQDQNF
Consensus             (51) E QILRLLSNSPLQVDITLLRIDSH SKNTP EHL  FY TFEEIKDQKF

                           101                                                150
MetA_B.halodurans    (101) MGMIITGAPIETLPYDEVDYWNELKQIMEWSKTNVTSTLHICWGAQAGLF
MetA_B.subtilis      (101) LMMIITGAPIEHLAFEEVSYWEELKEIMEWSKTNVTSTLHICWGAQAGLY
MetA_Bruc.meritensis (101) LFVITGAPVERLPFEEVTYWDEMRRVFDWTQSHVHRTLNICWAAQAAVY
MetA_C.acetobutylicum(101) MIVTGAPVETLSFENVDYWEELCRIFDWSVTNVTSTIHICWGAQAGLY
MetA_Camp.jejuni     (100) AIVTGAPVEQMDFEKVAYWEELLEIFDFLKQNVTSSMYICWGAMAALK
MetA_E.coli          (101) LIVTGAPLGLVEFNDVAYWPQIKQVLEWSKDHVTSTLFVCWAVQAALN
MetA_L.lactis        (101) LIVTGAPVEQLNFEEVDYWSELLKIIDWSKSHVYSSLHICWAAQAALY
MetA_R.meliloti      (101) FIITGAPIETLEYEEVTYWKELQRIFDWTTTNVHSTLNVCWGGMAAVY
MetA_S.typhi         (101) LIVTGAPLGLVEFNDVAYWPQIRQVLEWAKDHVTSTLFVCWAVQAALN
MetA_S.typhimurium   (101) LIVTGAPLGLVEFNDVAYWPQIRQVLEWAKDHVTSTLFVCWAVQAALN
MetA_Str.pneumoniae  (101) MIITGAPVEHLPFEEVDYWEEFRQMLEWSKTHVYSTLHICWGAQAGLY
MetA_T.maritima      (101) FIITGAPVELLPFEEVDYWEELTEIMEWSRHNVYSTMFICWAAQAGLY
MetA_V.cholerae      (101) LIITGAPLGLVQFEDVAYWQHLQNIMAWAKAHVTSTLYICWAAQAGLK
MetA_Y.pestis        (101) LIVTGAPLGLVDFCDVAYWPQIERIIAWAKEHVTSTLFVCWAVQAALN
Consensus            (101) GLIITGAPVE L FEEVAYW ELR ILEWSKTHVTSTLHICWAAQAALY

                           151                                                200
MetA_B.halodurans    (151) YHYGVEKVPLPEKQFGVYPHKINVPNVKLLRGFDDEFYVPHSRHTDINKA
MetA_B.subtilis      (151) YHYGVEKIQMPKKIFGVFEHTVLSKHERLVRGFDELYYVPHSRHTDINME
MetA_Bruc.meritensis (151) HFHGMKKYDLPAKASGVFRQRSLVLASPYLRGFSDDFAIPVSRWTEVRKS
MetA_C.acetobutylicum(151) HHYGIPKYELHEKLFGVYKHNLTERNIKLTRGFDDEFYAPHSRHTYVKRE
MetA_Camp.jejuni     (150) YFYGVDKISLDKKIFGVYKHDKVSPDLLLTN-LDEKVLMPHSRHSSMDEE
MetA_E.coli          (151) ILYGIPKQTRTEKLSGVYEHHILHPHALLTRGFDDSFLAPHSRYADFPAA
MetA_L.lactis        (151) ARYGVTKENLPQKLCGIYKSSVEQPKNPLFRGFDDFFNYPQSRYTQSNPS
MetA_R.meliloti      (151) HFHGVPKYPLKEKAFGVYRHQNLQPSSVYLNGFSDDFAVPVSRWTEVRRA
MetA_S.typhi         (151) ILYGIPKQTRTDKLSGVYEHHILHPHALLTRGFDDSFLAPHSRYADFPAA
MetA_S.typhimurium   (151) ILYGIPKQTRTDKLSGVYEHHILHPHALLTRGFDDSFLAPHSRYADFPAA
MetA_Str.pneumoniae  (151) LRYGVEKYQMDSKLSGIYPQDTLKEGHLLFRGFDDSYVSPHSRHTEISKE
MetA_T.maritima      (151) YFYGIPKYELPQKLSGVYKHR-VAKDSVLFRGHDDFFWAPHSRYTEVKKE
MetA_V.cholerae      (151) LLYNLPKRTREEKLSGVYYHDIHKPFHPLLRGFDDRFLAPHSRYADFDAE
MetA_Y.pestis        (151) ILYGIPKMTREVKLSGIYQHQTLEPLALLTRGFDETFLAPHSRYADFPVE
Consensus            (151) Y YGIPK  L EKLSGVY H IL P ALL RGFDD FLAPHSRYTDV  E

                           201                                                250
MetA_B.halodurans    (201) QIEAHPDLEILSESEQ-AGVYIVASKDGKQIFVTGHSEYDACTLQQEYER
MetA_B.subtilis      (201) QLQAVPELNILTASKEAGGLLLIVSKDEKQVFLTGHPEYDTNTLLQEYER
MetA_Bruc.meritensis (201) DIPADSGLKVLVDSTE-TGLCLLDDPRHRSLHMFNHVEYDTTSLADEYFR
MetA_C.acetobutylicum(201) DIKKNPSLKILAESDE-AGAYIVASENGKNIFVMGHAEYDGDTLNLEYIR
MetA_Camp.jejuni     (199) QILALQKQGKLKILLRNKKIGSALLRDEKNIFILGHLEYFKETLHQEYVR
MetA_E.coli          (201) LIRDYTDLEILAETEE-GDAYLFASKDKRIAFVTGHPEYDAQTLAQEFFR
MetA_L.lactis        (201) EIKKVPDLEVLSSSKE-TGFSILAKKNLREIYLFGHLEYDRETIAWEYER
MetA_R.meliloti      (201) DIDRVPDLEILMESKE-VGVCLVHEKKGNRLYMFNHVEYDSTSLSEEYFR
MetA_S.typhi         (201) LIRDYTDLEILAETEE-GDAYLFASKDKRIAFVTGHPEYDAHTLAGEYFR
MetA_S.typhimurium   (201) LIRDYTDLEILAETEE-GDAYLFASKDKRIAFVTGHPEYDAHTLAGEYFR
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MetA_Str.pneumoniae   (201) EVLNKTNLEILSEGPQ-VGVSILASRDLREIYSFGHLEYDRDTLAKEYFR
      MetA_T.maritima   (200) DIDKVPELEILAESDE-AGVYVVANKSERQIFVTGHPEYDRYTLRDEYYR
      MetA_V.cholerae   (201) FLAEHTDLDILATSDV-AGVYLAATKDKRNVFVTGHPEYDAYTLHGEYVR
        MetA_Y.pestis   (201) VLQQYTDLDILVSSEE-AGAYLFASKDKRVAFVTGHPEYDVDTLAGEYQR
            Consensus   (201) I    TDLEILAESEE AGVYLVASKD R IFVTGHPEYD  TLA EYFR
                               251                                              300
     MetA_B.halodurans  (250) DRAR-GLNIQVPENYFPNDDATRKPLLRWRAHSYLLFSNWLNYYV  ETP
       MetA_B.subtilis  (251) DLERNLSTVEAPKHYFAKGSNE--PVNRWKAHATLLFMNWLNYYV  ETP
    MetA_Bruc.meritensis (250) DIQV-QPEAKVPVNYFPGDDAKRPPENRWRSHAHLLFGNWIN-EM  STP
  MetA_C.acetobutylicum (250) DKNQ-GMNIKIPKNYFKDNDPEKGPMVTWRGHANLLFSNWLNYYV  ETP
      MetA_Camp.jejuni  (249) --D--N-FIQKAKNYYDKKGN---IKYNWRSNANTIFANWLNYDV  STP
           MetA_E.coli  (250) DVEA-GLDPDVPYNYFPHNDPQNTPRASWRSHGNLLFTNWLNYYV  ITP
         MetA_L.lactis  (250) DKEE-GLKPNLPQNYFPENDDKNKPKSTWASAASLFFSNWLNYAV  GTP
       MetA_R.meliloti  (250) DVDA-GVPIKLPHDYFPHNDSALPPQNRWRSHAHLFFGNWIN-EI  TTP
          MetA_S.typhi  (250) DVEA-GLNPEIPYNYFPKNDPQSIPRTTWRSHGNLLFTNWLNYYV  ITP
    MetA_S.typhimurium  (250) DVEA-GLNPEVPYNYFPKNDPQNIPRATWRSHGNLLFTNWLNYYV  ITP
   MetA_Str.pneumoniae  (250) DRDA-GFDPHIPENYFKDDDVNQVPCLCWSSSAALFFSNWVDHAV  ETP
       MetA_T.maritima  (249) DIGR-NLKVPIPANYFPNDDPTKTPILTWWSHAHLFFSNWLNYCI  KTP
       MetA_V.cholerae  (250) DLGE-GLNPAIPVNYYPNDNPDNKPCASWRSHGHLLFANWLNYCV  QTP
         MetA_Y.pestis  (250) DLAA-GLNPQVPLNYFPSDDASLRPKASWRSHGHLLFANWLNYAV  ITP
            Consensus   (251) DVE  GL P IP NYFP  D   P   TWRSHA LLFSNWLNYV   TP
                               301                   323
     MetA_B.halodurans  (299) YDLSR------------------
       MetA_B.subtilis  (299) YEWD-------------------
    MetA_Bruc.meritensis (298) YDIERIGKV--------------
  MetA_C.acetobutylicum (299) FEL--------------------
      MetA_Camp.jejuni  (291) FVL--------------------
           MetA_E.coli  (299) YDLRHMNPTLD------------
         MetA_L.lactis  (299) YLGERLSQHLNEENYDFNQKEQK
       MetA_R.meliloti  (298) YELAKIGTGER------------
          MetA_S.typhi  (299) YDLRHMNPTLD------------
    MetA_S.typhimurium  (299) YDLRHMNPTLD------------
   MetA_Str.pneumoniae  (299) FDWRKIEDDASAYGYL-------
       MetA_T.maritima  (298) YRLEDIH----------------
       MetA_V.cholerae  (299) YDLEKFSEANFTKDE--------
         MetA_Y.pestis  (299) FDLRHMNPTLD------------
            Consensus   (301) YDL  I
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